

0550
11/06

#3

OIPE

RAW SEQUENCE LISTING

DATE: 11/12/2001

PATENT APPLICATION: US/09/934,060A

TIME: 19:10:18

Input Set : A:\144 Sequence Listing_resubmit.txt

Output Set: N:\CRF3\11122001\I934060A.raw

3 <110> APPLICANT: DeVico, Anthony L.
4 Fouts, Timothy R.
5 Tuskan, Robert G.
7 <120> TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE
9 <130> FILE REFERENCE: 4115-144 CIP
11 <140> CURRENT APPLICATION NUMBER: US 09/934,060A
12 <141> CURRENT FILING DATE: 2001-08-21
14 <150> PRIOR APPLICATION NUMBER: US 09/684,026
15 <151> PRIOR FILING DATE: 2000-10-06
17 <150> PRIOR APPLICATION NUMBER: US 60/158,321
18 <151> PRIOR FILING DATE: 1999-10-08
20 <160> NUMBER OF SEQ ID NOS: 33
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2159
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Synthesized construct
32 <400> SEQUENCE: 1

ENTERED
P. 5

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37 tggaaggagg ccaccaccac cctgttctgc gccagcgacc gcaaggccta cgacaccgag 180
39 gtgcacaacg tgtggggccac ccacgcctgc gtgcccaccg accccaaccc ccaggagggtg 240
41 gagctgaaga acgtgaccga gaacttcaac atgtggaaga acaacatggt ggagcagatg 300
43 cagcaggaca tcatcagcct gtgggaccag agcctgaagc cctgcgtgaa gctgaccccc 360
45 ctgtgcgtga ccctgaactg caccgacctg cgcaacgcca ccaacggcaa cgacaccaac 420
47 accactagta gcagccgcgg catggtgggg ggcggcgaga tgaagaactg cagcttcaac 480
49 atcaccacca acatccgcgg caaggtgcag aaggagtacg cctgttcta caagctggac 540
51 atcgccccc a tcgacaacaa cagcaacaac cgctaccgcc tgatcagctg caacaccagc 600
53 gtgatcacc c aggcctgccc caaggtgagc ttcgagccca tccccatcca ctactgcgcc 660
55 cccgccggct tcgccatcct gaagtgcagg gacaagaagt tcaacggcaa gggcccctgc 720
57 accaacgtga gcaccgtgca gtgcacccac ggcacccgcc ccgtggtgag caccagctg 780
59 ctgctgaacg gcagcctggc cgaggaggag gtggtgatcc gcagcgccaa cttcgccgac 840
61 aacgccaaag tgatcatcgt gcagctgaac gagagcgtgg agatcaactg caccgcgcc 900
63 aacaacaaca cccgcaagtc catccacatc ggcgccggcc gcgccttcta caccaccggc 960
65 gagatcatcg gcgacatccg ccaggccacc tgcaacctga gccgcgccaa gtggaacgac 1020
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69 aagcacagca gcggcgggcg ccccgagatc gtgacccaca gtttcaattg cggcgggcag 1140
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79 gaggtgttcc gccccggcgg cggcgacatg cgcgacaact ggcgcagcga gctgtacaag 1440
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83 gtgcagcgcg agaagcgtgg atcctctggt ggcggtggct cgggctccgg aggaggtgg 1560
85 tcgggtggcg gcgcggccgc taagaaagtg gtgctgggca aaaaagggga tacagtggaa 1620

Not Entered

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87 ctgacctgta cagcttccca gaagaagagc atacaattcc actggaaaaa ctccaaccag 1680
89 ataaagattc tgggaaatca gggctccttc ttaactaaag gtccatccaa gctgaatgat 1740
91 cgcgctgact caagaagaag cctttgggac caaggaaact tccccctgat catcaagaat 1800
93 ctttaagatag aagactcaga tacttacatc tgtgaagtgg aggaccagaa ggaggagggtg 1860
95 caattgctag tgttcgatt gactgccaac tctgacaccc acctgcttca ggggcagagc 1920
97 ctgaccctga ccttggagag cccccctggt agtagcccct cagtgcattg taggagtcca 1980
99 aggggtaaaa acatacaggg ggggaagacc ctctccgtgt ctcagctgga gctccaggat 2040
101 agtggcacct ggacatgcac tgtcttgagc aaccagaaga aggtggagtt caaaatagac 2100
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112 <223> OTHER INFORMATION: Synthesized construct ✓
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120 <220> FEATURE:
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122 <222> LOCATION: (719)..(719)
123 <223> OTHER INFORMATION: Xaa can be any amino acid
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133 20 25 30
136 Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
137 35 40 45
140 Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
141 50 55 60
144 Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
145 65 70 75 80
148 Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
149 85 90 95
152 Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
153 100 105 110
156 Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
157 115 120 125
160 Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
161 130 135 140
164 Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
165 145 150 155 160
168 Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
169 165 170 175
172 Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
173 180 185 190
176 Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys

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Input Set : A:\144 Sequence Listing_resubmit.txt

Output Set: N:\CRF3\11122001\I934060A.raw

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180 Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
181          210          215          220
184 Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys
185 225          230          235          240
188 Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val
189          245          250          255
192 Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
193          260          265          270
196 Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln
197          275          280          285
200 Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
201          290          295          300
204 Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly
205 305          310          315          320
208 Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala
209          325          330          335
212 Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln
213          340          345          350
216 Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro
217          355          360          365
220 Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
221          370          375          380
224 Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser
225 385          390          395          400
228 Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys
229          405          410          415
232 Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro
233          420          425          430
236 Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
237          435          440          445
240 Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg
241          450          455          460
244 Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
245 465          470          475          480
248 Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
249          485          490          495
252 Lys Arg Arg Val Val Gln Arg Glu Lys Arg Gly Ser Ser Gly Gly Gly
253          500          505          510
256 Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys
257          515          520          525
260 Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr
261          530          535          540
264 Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln
265 545          550          555          560
268 Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser
269          565          570          575
272 Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly
273          580          585          590

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276 Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr
277          595          600          605
280 Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val
281      610          615          620
284 Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser
285 625          630          635          640
288 Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln
289          645          650          655
292 Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser
293          660          665          670
296 Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val
297          675          680          685
300 Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu
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W--> 304 Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Tyr Val Xaa Thr
305 705          710          715          720
308 <210> SEQ ID NO: 3
309 <211> LENGTH: 2159
310 <212> TYPE: DNA
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321 tggaaggagg ccaccaccac cctgtttctgc gccagcgacc gcaaggccta cgacaccgag      180
323 gtgcacaacg tgtgggccac ccacgcctgc gtgcccaccg accccaaccc ccaggaggtg      240
325 gagctgaaga acgtgaccga gaacttcaac atgtggaaga acaacatggt ggagcagatg      300
327 cacgaggaca tcatcagcct gtgggaccag agcctgaagc cctgcgtgaa gctgaccccc      360
329 ctgtgcgtga ccctgaactg caccgacctg cgcaacgcca ccaacggcaa cgacaccaac      420
331 accactagta gcagccgcgg catggtgggc ggcggcgaga tgaagaactg cagcttcaac      480
333 atcaccacca acatccgcgg caaggtgcag aaggagtacg ccctgttcta caagctggac      540
335 atcgcccca tcgacaacaa cagcaacaac cgctaccgcc tgatcagctg caacaccagc      600
337 gtgatcacc aggcctgccc caaggtgagc ttcgagccca tccccatcca ctactgcgc      660
339 cccgccggt tcgccatcct gaagtgaag gacaagaagt tcaacggcaa gggcccctgc      720
341 accaacgtga gcaccgtgca gtgcaccac ggcacccgcc ccgtggtgag caccagctg      780
343 ctgctgaacg gcagcctggc cgaggaggag gtggtgatcc gcagcgcaa cttcgccgac      840
345 aacgccaagg tgatcatcgt gcagctgaac gagagcgtgg agatcaactg caccgcccc      900
347 aacaacaaca cccgcaagtc catccacatc ggcgccggcc gcgccttcta caccaccggc      960
349 gagatcatcg gcgacatccg ccaggccac tgcaacctga gccgcgcaa gtggaacgac      1020
351 accctgaaca agatcgtgat caagctgcgc gagcagttcg gcaacaagac catcgtgttc      1080
353 aagcacagca gcggcggcga ccccgagatc gtgaccacaa gcttcaattg cggcggcgag      1140
355 ttctttact gcaacagcac ccagctgttc aacagcacct ggaacgtgac cgaggagagc      1200
357 aacaacaccg tggaagaaca caccatcacc ctgccctgcc gcatcaagca gatcatcaac      1260
359 atgtggcagg aggtggggcg cgcctgttac gccccccca tccgcggcca gatccgctgc      1320
361 agttchaaca tcaccggcct gctgctgacc cgcgacggcg gccccgagga caacaagacc      1380
363 gagtggttcc gccccggcgg cggcgacatg cgcgacaact ggcgcagcga gctgtacaag      1440
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369 tcgggtggcg ggcgcggccgc taagaaagtg gtgctgggca aaaaagggga tacagtggaa 1620
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373 ataaagattc tgggaaatca gggctccttc ttaactaaag gtccatccaa gctgaatgat 1740
375 cgcgctgact caagaagaag cctttgggac caaggaaact tccccctgat catcaagaat 1800
377 cttaagatag aagactcaga tacttacatc tgtgaagtgg aggaccagaa ggaggaggtg 1860
379 caattgctag tgttcggatt gactgccaac tctgacaccc acctgcttca ggggcagagc 1920
381 ctgaccctga ccttggagag cccccctggt agtagccoct cagtgcaatg taggagtcca 1980
383 aggggtaaaa acatacaggg ggggaagacc ctctccgtgt ctcagctgga gctccaggat 2040
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396 <223> OTHER INFORMATION: Synthesized construct
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399 <221> NAME/KEY: MISC_FEATURE
400 <222> LOCATION: (716)..(716)
401 <223> OTHER INFORMATION: Xaa can be any amino acid
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406 <222> LOCATION: (719)..(719)
407 <223> OTHER INFORMATION: Xaa can be any amino acid
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417 20 25 30
420 Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
421 35 40 45
424 Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
425 50 55 60
428 Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
429 65 70 75 80
432 Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
433 85 90 95
436 Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
437 100 105 110
440 Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
441 115 120 125
444 Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
445 130 135 140
448 Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
449 145 150 155 160
452 Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
453 165 170 175
456 Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
457 180 185 190

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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
listing n or Xaa.

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
listing n or Xaa.

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
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VERIFICATION SUMMARY

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L:588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 -
L:810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 -
L:1140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 -
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 -
L:2040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 -